

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Ullrich, Axel  
Gishizsky, Mikhail  
Sures, Irman G.

(ii) TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine Kinases

(iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: U.S.A.  
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/426,509  
(B) FILING DATE: 21-APR-1995  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/282,545  
(B) FILING DATE: 22-APR-1994  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Coruzzi, Laura A.  
(B) REGISTRATION NUMBER: 30,742  
(C) REFERENCE/DOCKET NUMBER: 7683-074

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212)790-9090  
(B) TELEFAX: (212)869-9741  
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2000 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGCTCCAA GTTGTGCAGC CGGGACCGCC TCGGGGTGTG CAGCCGGCTC GCGGAGGCCC 60  
TCCTGGGGGC GGGCGCGGGG CGGCTCGGGG GCGCCCCCTG AGCAGAAAAC AGGAAGAACC 120  
AGGCTCGGTC CAGTGGCACC CAGCTCCCTA CCTCCTGTGC CAGCCGCCTG GCCTGTGGCA 180  
GGCCATTCCC AGCGTCCCCG ACTGTGACCA CTTGCTCAGT GTGCCTCTCA CCTGCCTCAG 240  
TTTCCCTCTG GGGGGCGATG GCGGGGCGAG GCTCTCTGGT TTCCTGGCGG GCATTTTCAG 300  
GCTGTGATTG TGCTGAGGAA CTTCCCCGGG TGAGCCCCCG CTTCTCCGA GCCTGGCACC 360  
CCCCTCCCGT CTCAGCCAGG ATGCCAACGA GCGGCTGGGC CCCGGGCACC CAGTGTATCA 420  
CCAAATGCGA GCACACCCGC CCCAAGCCAG GGGAGCTGGC CTTCCGCAAG GCGGACGTGG 480  
TCACCATCCT GGAGGCCTGC GAGAAACAAGA GCTGGTACCG CGTCAAGCAC CACACCAGTG 540  
GACAGGAGGG GCTGCTGGCA GCTGGGCGCG TGCGGGAGCG GGAGGCCCTC TCCGCAGACC 600  
CCAAGCTCAG CCTCATGCCG TGGTTCCACG GGAAGATCTC GGGCCAGGAG GCTGTCCAGC 660  
AGCTGCAGCC TCCCGAGGAT GGGCTGTTCC TGGTGCGGGA GTCCGCGCGC CACCCCGCGC 720  
ACTACGTCCT GTGCGTGAGC TTTGGCCGCG ACGTGATCCA CTACCGCGTG CTGCACCGCG 780  
ACGGCCACCT CACAATCGAT GAGGCCGTGT TCTTCTGCAA CCTCATGGAC ATGGTGGAGC 840  
ATTACAGCAA GGACAAGGGC GCTATCTGCA CCAAGCTGGT GAGACCAAAG CGGAAACACG 900  
GGACCAAGTC GGCCGAGGAG GAGCTGGCCA GGGCGGGCTG GTTACTGAAC CTGCAGCATT 960  
TGACATTGGG AGCACAGATC GGAGAGGGAG AGTTTGAGC TGTCTGCAG GGTGAGTACC 1020  
TGGGGCAAAA GGTGGCCGTG AAGAATATCA AGTGTGATGT GACAGCCCAG GCCTTCCTGG 1080  
ACGAGACGGC CGTCATGACG AAGATGCAAC ACGAGAACCT GGTGCGTCTC CTGGGCGTGA 1140  
TCCTGCACCA GGGGCTGTAC ATTGTCATGG AGCACGTGAG CAAGGGCAAC CTGGTGAAC 1200  
TTCTGCGGAC CCGGGGTCGA GCCCTCGTGA ACACCGCTCA GCTCCTGCAG TTTTCTCTGC 1260  
ACGTGGCCGA GGGCATGGAG TACCTGGAGA GCAAGAAGCT TGTGCACCGC GACCTGGCCG 1320  
CCCGCAACAT CCTGGTCTCA GAGGACCTGG TGGCCAAGGT CAGCGACTTT GGCCTGGCCA 1380  
AAGCCGAGCG GAAGGGGCTA GACTCAAGCC GGCTGCCCCT CAAGTGGACG GCGCCCGAGG 1440  
CTCTCAAACA CGGGAAGTTC ACCAGCAAGT CGGATGTCTG GAGTTTGGG GTGCTGCTCT 1500  
GGGAGGTCTT CTCATATGGA CGGGCTCCGT ACCCTAAAAT GTCAGTAAA GAGGTGTCGG 1560  
AGGCCGTGGA GAAGGGGTAC CGCATGGAAC CCCCCGAGGG CTGTCCAGGC CCCGTGCACG 1620  
TCCTCATGAG CAGCTGCTGG GAGGCAGAGC CCGCCCGCCG GCCACCCTTC CGCAAACCTGG 1680  
CCGAGAAGCT GGCCCGGGAG CTACGCAGTG CAGGTGCCCC AGCCTCCGTC TCAGGGCAGG 1740  
ACGCCGACGG CTCCACCTCG CCCCGAAGCC AGGAGCCCTG ACCCCACCCG GTGGGGCCCT 1800  
TGGCCCCAGA GGACCGAGAG AGTGGAGAGT GCGGCGTGGG GGCAGTACC AGGCCCAAGG 1860  
AGGGTCCAGG CGGGCAAGTC ATCCTCCTGG TGCCACAGC AGGGGCTGGC CCACGTAGG 1920

A

GGCTCTGGGC GGCCCGTGGA CACCCAGAC CTGCGAAGGA TGATCGCCCG ATAAAGACGG 1980  
ATTCTAAGGA CTCTAAAAAA 2000

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Gly	Arg	Gly	Ser	Leu	Val	Ser	Trp	Arg	Ala	Phe	His	Gly	Cys	
1				5					10					15		
Asp	Ser	Ala	Glu	Glu	Leu	Pro	Arg	Val	Ser	Pro	Arg	Phe	Leu	Arg	Ala	
		20					25					30				
Trp	His	Pro	Pro	Pro	Val	Ser	Ala	Arg	Met	Pro	Thr	Arg	Arg	Trp	Ala	
		35					40					45				
Pro	Gly	Thr	Gln	Cys	Ile	Thr	Lys	Cys	Glu	His	Thr	Arg	Pro	Lys	Pro	
	50					55					60					
Gly	Glu	Leu	Ala	Phe	Arg	Lys	Gly	Asp	Val	Val	Thr	Ile	Leu	Glu	Ala	
65					70				75					80		
Cys	Glu	Asn	Lys	Ser	Trp	Tyr	Arg	Val	Lys	His	His	Thr	Ser	Gly	Gln	
			85						90					95		
Glu	Gly	Leu	Leu	Ala	Ala	Gly	Ala	Leu	Arg	Glu	Arg	Glu	Ala	Leu	Ser	
			100					105					110			
Ala	Asp	Pro	Lys	Leu	Ser	Leu	Met	Pro	Trp	Phe	His	Gly	Lys	Ile	Ser	
		115					120					125				
Gly	Gln	Glu	Ala	Val	Gln	Gln	Leu	Gln	Pro	Pro	Glu	Asp	Gly	Leu	Phe	
	130					135					140					
Leu	Val	Arg	Glu	Ser	Ala	Arg	His	Pro	Gly	Asp	Tyr	Val	Leu	Cys	Val	
145					150					155				160		
Ser	Phe	Gly	Arg	Asp	Val	Ile	His	Tyr	Arg	Val	Leu	His	Arg	Asp	Gly	
			165						170				175			
His	Leu	Thr	Ile	Asp	Glu	Ala	Val	Phe	Phe	Cys	Asn	Leu	Met	Asp	Met	
			180					185					190			
Val	Glu	His	Tyr	Ser	Lys	Asp	Lys	Gly	Ala	Ile	Cys	Thr	Lys	Leu	Val	
		195					200					205				
Arg	Pro	Lys	Arg	Lys	His	Gly	Thr	Lys	Ser	Ala	Glu	Glu	Glu	Leu	Ala	
	210					215					220					
Arg	Ala	Gly	Trp	Leu	Leu	Asn	Leu	Gln	His	Leu	Thr	Leu	Gly	Ala	Gln	
225					230					235					240	

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Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln Gly Glu Tyr Leu Gly  
 245 250 255  
 Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp Val Thr Ala Gln Ala  
 260 265 270  
 Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met Gln His Glu Asn Leu  
 275 280 285  
 Val Arg Leu Leu Gly Val Ile Leu His Gln Gly Leu Tyr Ile Val Met  
 290 295 300  
 Glu His Val Ser Lys Gly Asn Leu Val Asn Phe Leu Arg Thr Arg Gly  
 305 310 315 320  
 Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln Phe Ser Leu His Val  
 325 330 335  
 Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys Leu Val His Arg Asp  
 340 345 350  
 Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp Leu Val Ala Lys Val  
 355 360 365  
 Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys Gly Leu Asp Ser Ser  
 370 375 380  
 Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Lys His Gly Lys  
 385 390 395 400  
 Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu  
 405 410 415  
 Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys Met Ser Leu Lys Glu  
 420 425 430  
 Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met Glu Pro Pro Glu Gly  
 435 440 445  
 Cys Pro Gly Pro Val His Val Leu Met Ser Ser Cys Trp Glu Ala Glu  
 450 455 460  
 Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala Glu Lys Leu Ala Arg  
 465 470 475 480  
 Glu Leu Arg Ser Ala Gly Ala Pro Ala Ser Val Ser Gly Gln Asp Ala  
 485 490 495  
 Asp Gly Ser Thr Ser Pro Arg Ser Gln Glu Pro  
 500 505

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGCTTTTTG	CTTAGAGCTT	GAGAGTCAAA	GTTAAGGACC	CACATGTATA	CTTCGGCTCT	60
AGCGAGTCTA	AGGATGATAA	TATGGATACA	AAATCTATTC	TAGAAGAACT	TCTTCTCAAA	120
AGATCACAGC	AAAAGAAGAA	AATGTCACCA	AATAATTACA	AAGAACGGCT	TTTTGTTTTG	180
ACCAAAACAA	ACCTTTCCTA	CTATGAATAT	GACAAAATGA	AAAGGGGCAG	CAGAAAAGGA	240
TCCATTGAAA	TTAAGAAAAT	CAGATGTGTG	GAGAAAGTAA	ATCTCGAGGA	GCAGACGCCT	300
GTAGAGAGAC	AGTACCCATT	TCAGATTGTC	TATAAAGATG	GGCTTCTCTA	TGTCCTATGCA	360
TCAAATGAAG	AGAGCCGAAG	TCAGTGGTTG	AAAGCATTAC	AAAAAGAGAT	AAGGGGTAAC	420
CCCCACCTGC	TGGTCAAGTA	CCATAGTGGG	TTCTTCGTGG	ACGGGAAGTT	CCTGTGTTGC	480
CAGCAGAGCT	GTAAAGCAGC	CCAGGATGT	ACCCTCTGGG	AAGCATATGC	TAATCTGCAT	540
ACTGCAGTCA	ATGAAGAGAA	ACACAGAGTT	CCCACCTTCC	CAGACAGAGT	GCTGAAGATA	600
CCTCGGGCAG	TTCCTGTTCT	CAAAATGGAT	GCACCATCTT	CAAGTACCAC	TCTAGCCCAA	660
TATGACAACG	AATCAAAGAA	AACTATGGC	TCCCAGCCAC	CATCTTCAAG	TACCAGTCTA	720
GCGCAATATG	ACAGCAACTC	AAAGAAAATC	TATGGCTCCC	AGCCAAACTT	CAACATGCAG	780
TATATTCCAA	GGGAAGACTT	CCCTGACTGG	TGGCAAGTAA	GAAAACTGAA	AAGTAGCAGC	840
AGCAGTGAAG	ATGTTGCAAG	CAGTAACCAA	AAAGAAAGAA	ATGTGAATCA	CACCACCTCA	900
AAGATTTTCA	GGGAATTCCC	TGAGTCAAGT	TCATCTGAAG	AAGAGGAAAA	CCTGGATGAT	960
TATGACTGGT	TTGCTGGTAA	CATCTCCAGA	TCACAATCTG	AACAGTTACT	CAGACAAAAG	1020
GGAAAAGAAG	GAGCATTTAT	GGTTAGAAAT	TCGAGCCAAG	TGGGAATGTA	CACAGTGTCC	1080
TTATTTAGTA	AGGCTGTGAA	TGATAAAAAA	GGAAGTGTCA	AACATTACCA	CGTGCATACA	1140
AATGCTGAGA	ACAAATTATA	CCTGGCAGAA	AACTACTGTT	TTGATTCCAT	TCCAAAGCTT	1200
ATTCATTATC	ATCAACACAA	TTCAGCAGGC	ATGATCACAC	GGCTCCGCCA	CCCTGTGTCA	1260
ACAAAGGCCA	ACAAGGTCCC	CGACTCTGTG	TCCCTGGGAA	ATGGAATCTG	GGAAGTGAAG	1320
AGAGAAGAGA	TTACCTTGTT	GAAGGAGCTG	GGAAGTGGCC	AGTTTGGAGT	GGTCCAGCTG	1380
GGCAAGTGGA	AGGGGCAGTA	TGATGTTGCT	GTTAAGATGA	TCAAGGAGGG	CTCCATGTCA	1440
GAAGATGAAT	TCTTTCAGGA	GGCCAGACT	ATGATGAAAC	TCAGCCATCC	CAAGCTGGTT	1500
AAATTCTATG	GAGTGTGTTT	AAAGGAATAC	CCCATATACA	TAGTGACTGA	ATATATAAGC	1560
AATGGCTGCT	TGCTGAATTA	CCTGAGGAGT	CACGGAAAAG	GAAGTGAACC	TTCCCAGCTC	1620
TTAGAAATGT	GCTACGATGT	CTGTGAAGGC	ATGGCCTTCT	TGGAGAGTCA	CCAATTCATA	1680
CACCGGGACT	TGGCTGCTCG	TAACTGCTTG	GTGGACAGAG	ATCTCTGTGT	GAAAGTATCT	1740
GACTTTGGAA	TGACAAGGTA	TGTTCTTGAT	GACCAGTATG	TCAGTTCAGT	CGGAACAAAG	1800
TTTCCAGTCA	AGTGGTCAGC	TCCAGAGGTG	TTTCATTACT	TCAAATACAG	CAGCAAGTCA	1860

10

GACGTATGGG CATTGTTGGGAT CCTGATGTGG GAGGTGTTCA GCCTGGGGAA GCAGCCCTAT 1920  
 GACTTGTATG ACAACTCCCA GGTGGTTCTG AAGGTCTCCC AGGGCCACAG GCTTTACCGG 1980  
 CCCCACCTGG CATCGGACAC CATCTACCAG ATCATGTACA GCTGCTGGCA CGAGCTTCCA 2040  
 GAAAAGCGTC CCACATTTCA GCAACTCCTG TCTTCCATTG AACCACTTCG GGAAAAAGAC 2100  
 AAGCATTGAA GAAGAAATTA GGAGTGCTGA TAAGAATGAA TATAGATGCT GGCCAGCATT 2160  
 TTCATTCAATT TTAAGGAAAG TAGCAAGGCA TAATGTAATT TAGCTAGTTT TTAATAGTGT 2220  
 TCTCTGTATT GTCTATTATT TAGAAATGAA CAAGGCAGGA AACAAAAGAT TCCCTTGAAA 2280  
 TTTAGGTCAA ATTAGTAATT TTGTTTATGC TGCCCCTGAT ATAACACTTT CCAGCCTATA 2340  
 GCAGAAGCAC ATTTTCAGAC TGCAATATAG AGACTGTGTT CATGTGTAAA GACTGAGCAG 2400  
 AACTGAAAAA TTACTTATTG GATATTCATT CTTTTCTTTA TATTGTCATT GTCACAACAA 2460  
 TTAAATATAC TACCAAGTAC AAAAAAAAAA AAAAAAAAAA 2500

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 675 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Thr Lys Ser Ile Leu Glu Glu Leu Leu Lys Arg Ser Gln  
 1 5 10 15  
 Gln Lys Lys Lys Met Ser Pro Asn Asn Tyr Lys Glu Arg Leu Phe Val  
 20 25 30  
 Leu Thr Lys Thr Asn Leu Ser Tyr Tyr Glu Tyr Asp Lys Met Lys Arg  
 35 40 45  
 Gly Ser Arg Lys Gly Ser Ile Glu Ile Lys Lys Ile Arg Cys Val Glu  
 50 55 60  
 Lys Val Asn Leu Glu Glu Gln Thr Pro Val Glu Arg Gln Tyr Pro Phe  
 65 70 75 80  
 Gln Ile Val Tyr Lys Asp Gly Leu Leu Tyr Val Tyr Ala Ser Asn Glu  
 85 90 95  
 Glu Ser Arg Ser Gln Trp Leu Lys Ala Leu Gln Lys Glu Ile Arg Gly  
 100 105 110  
 Asn Pro His Leu Leu Val Lys Tyr His Ser Gly Phe Phe Val Asp Gly  
 115 120 125  
 Lys Phe Leu Cys Cys Gln Gln Ser Cys Lys Ala Ala Pro Gly Cys Thr  
 130 135 140

A

Leu Trp Glu Ala Tyr Ala Asn Leu His Thr Ala Val Asn Glu Glu Lys  
 145 150 155 160  
 His Arg Val Pro Thr Phe Pro Asp Arg Val Leu Lys Ile Pro Arg Ala  
 165 170 175  
 Val Pro Val Leu Lys Met Asp Ala Pro Ser Ser Ser Thr Thr Leu Ala  
 180 185 190  
 Gln Tyr Asp Asn Glu Ser Lys Lys Asn Tyr Gly Ser Gln Pro Pro Ser  
 195 200 205  
 Ser Ser Thr Ser Leu Ala Gln Tyr Asp Ser Asn Ser Lys Lys Ile Tyr  
 210 215 220  
 Gly Ser Gln Pro Asn Phe Asn Met Gln Tyr Ile Pro Arg Glu Asp Phe  
 225 230 235 240  
 Pro Asp Trp Trp Gln Val Arg Lys Leu Lys Ser Ser Ser Ser Ser Glu  
 245 250 255  
 Asp Val Ala Ser Ser Asn Gln Lys Glu Arg Asn Val Asn His Thr Thr  
 260 265 270  
 Ser Lys Ile Ser Trp Glu Phe Pro Glu Ser Ser Ser Ser Glu Glu Glu  
 275 280 285  
 Glu Asn Leu Asp Asp Tyr Asp Trp Phe Ala Gly Asn Ile Ser Arg Ser  
 290 295 300  
 Gln Ser Glu Gln Leu Leu Arg Gln Lys Gly Lys Glu Gly Ala Phe Met  
 305 310 315 320  
 Val Arg Asn Ser Ser Gln Val Gly Met Tyr Thr Val Ser Leu Phe Ser  
 325 330 335  
 Lys Ala Val Asn Asp Lys Lys Gly Thr Val Lys His Tyr His Val His  
 340 345 350  
 Thr Asn Ala Glu Asn Lys Leu Tyr Leu Ala Glu Asn Tyr Cys Phe Asp  
 355 360 365  
 Ser Ile Pro Lys Leu Ile His Tyr His Gln His Asn Ser Ala Gly Met  
 370 375 380  
 Ile Thr Arg Leu Arg His Pro Val Ser Thr Lys Ala Asn Lys Val Pro  
 385 390 395 400  
 Asp Ser Val Ser Leu Gly Asn Gly Ile Trp Glu Leu Lys Arg Glu Glu  
 405 410 415  
 Ile Thr Leu Leu Lys Glu Leu Gly Ser Gly Gln Phe Gly Val Val Gln  
 420 425 430  
 Leu Gly Lys Trp Lys Gly Gln Tyr Asp Val Ala Val Lys Met Ile Lys  
 435 440 445  
 Glu Gly Ser Met Ser Glu Asp Glu Phe Phe Gln Glu Ala Gln Thr Met  
 450 455 460  
 Met Lys Leu Ser His Pro Lys Leu Val Lys Phe Tyr Gly Val Cys Ser  
 465 470 475 480

Lys Glu Tyr Pro Ile Tyr Ile Val Thr Glu Tyr Ile Ser Asn Gly Cys  
485 490 495

Leu Leu Asn Tyr Leu Arg Ser His Gly Lys Gly Leu Glu Pro Ser Gln  
500 505 510

Leu Leu Glu Met Cys Tyr Asp Val Cys Glu Gly Met Ala Phe Leu Glu  
515 520 525

Ser His Gln Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu Val  
530 535 540

Asp Arg Asp Leu Cys Val Lys Val Ser Asp Phe Gly Met Thr Arg Tyr  
545 550 555 560

Val Leu Asp Asp Gln Tyr Val Ser Ser Val Gly Thr Lys Phe Pro Val  
565 570 575

Lys Trp Ser Ala Pro Glu Val Phe His Tyr Phe Lys Tyr Ser Ser Lys  
580 585 590

Ser Asp Val Trp Ala Phe Gly Ile Leu Met Trp Glu Val Phe Ser Leu  
595 600 605

Gly Lys Gln Pro Tyr Asp Leu Tyr Asp Asn Ser Gln Val Val Leu Lys  
610 615 620

Val Ser Gln Gly His Arg Leu Tyr Arg Pro His Leu Ala Ser Asp Thr  
625 630 635 640

Ile Tyr Gln Ile Met Tyr Ser Cys Trp His Glu Leu Pro Glu Lys Arg  
645 650 655

Pro Thr Phe Gln Gln Leu Leu Ser Ser Ile Glu Pro Leu Arg Glu Lys  
660 665 670

Asp Lys His  
675

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGGACTGGT CGAAAGACAG GAACAGACTT GAAACAGGGG GAGAGCTCCT GCGAAACGA	60
AGACGTGGAG GTTTTACCAG GGATAAGAAG AAAAGACACC TTCCTAGTGA GCAGCTGCCC	120
AGCTCCTGCT CAGTTTTGCC TCGGGGTAGC ACCTCCAGCC ACAGAAAGCA AGCCGTAAG	180
TCTCTCCAGG TAGGACTTGC TGCAACCCAG CTGCTGGACT GATCTGAAAC GGGACTTTGC	240
ATACTCTCCG AAGTATGGTG AGTTGGTGCT GACTTCAAAG TTGCCTGGTG AAGGAAGATA	300

A



AGGTGGATCG CAGAGACTAA GGGGAGAGGG AGAAGCCCTG CTCCTCTTCT CCCACCAAG 360  
GCACAATGAG CAACATCTGT CAGAGGCTCT GGGAGTACCT AGAACCTAT CTCCCCTGTT 420  
TGTCCACGGA GGCAGACBAG TCAACCGTGA TTGAAAATCC AGGGGCCCTT TGCTCTCCCC 480  
AGTCACAGAG GCATGGCCAC TACTTTGTGG CTTTGTGTTGA TTACCAGGCT CGGACTGCTG 540  
AGGACTTGAG CTTCCGAGCA GGTGACAAAC TTCAAGTTCT GGACACTTTG CATGAGGGCT 600  
GGTGGTTTGC CAGACACTTG GAGAAAAGAC GAGATGGCTC CAGTCAGCAA CTACAAGGCT 660  
ATATTCCTTC TAACTACGTG GCTGAGGACA GAAGCCTACA GGCAGAGCCG TGGTTCTTTG 720  
GAGCAATCGG AAGATCAGAT GCAGAGAAAC AACTATTATA TTCAGAAAAC AAGACCGGTT 780  
CCTTTCTAAT CAGAGAAAGT GAAAGCCAAA AAGGAGAATT CTCTCTTTCA GTTTTAGATG 840  
GAGCAGTTGT AAAACACTAC AGAATTAATA GACTGGATGA AGGGGGATTT TTTCTCACGC 900  
GAAGAAGAAT CTTTTCAACA CTGAACGAAT TTGTGAGCCA CTACACCAAG ACAAGTGACG 960  
GCCTGTGTGT CAAGCTGGGG AAACCATGCT TAAAGATCCA GGTCCCAGCT CCATTTGATT 1020  
TGTCGTATAA AACCGTGGAC CAATGGGAGA TAGACCGCAA CTCCATACAG CTTCTGAAGC 1080  
GATTGGGATC TGGTCAGTTT GGCGAAGTAT GGGGAGGTCT GTGGAACAAT ACCACTCCAG 1140  
TAGCAGTGAA AACATTAAAA CCAGGTTCAA TGGATCAAA TGACTTCCTG AGGGAGGCAC 1200  
AGATAATGAA GAACCTAAGA CATCCAAAGC TTATCCAGCT TTATGCTGTT TGCACTTTAG 1260  
AAGATCCAAT TTATATTATT ACAGAGTTGA TGAGACATGG AAGTCTGCAA GAATATCTCC 1320  
AAAATGACAC TGGATCAAAA ATCCATCTGA CTCAACAGGT AGACATGGCG GCACAGGTTG 1380  
CCTCTGGAAT GGCCTATCTG GAGTCTCGGA ACTACATTCA CAGAGATCTG GCTGCCAGAA 1440  
ATGTCCTCGT TGGTGAACAT AATATCTACA AAGTAGCAGA TTTTGGACTT GCCAGAGTTT 1500  
TTAAGGTAGA TAATGAAGAC ATCTATGAAT CTAGACACGA AATAAAGCTG CCGGTGAAGT 1560  
GGACTGCGCC CGAAGCCATT CGTAGTAATA AATTCAGCAT TAAGTCCGAT GTATGGTCAT 1620  
TTGGAATCCT TCTTTATGAA ATCATTACTT ATGGCAAAAT GCCTTACAGT GGTATGACAG 1680  
GTGCCCAGGT AATCCAGATG TTGGCTCAA ACTATAGACT TCCGCAACCA TCCAAGTGC 1740  
CACAGCAATT TTACAACATC ATGTTGGAGT GCTGGAATGC AGAGCCTAAG GAACGACCTA 1800  
CATTTGAGAC ACTGCGTTGG AAACCTGAAG ACTATTTTGA AACAGACTCT TCATATTCAG 1860  
ATGCAAATAA CTTCATAAGA TGAACACTGG AGAAGAATAT CAAATAATAA AGTAGCAAAA 1920  
CAAATTCAAA TAATCCATT CAAAATACAA TGTTATCAAC CAACTGCACA ATCAGTTTAT 1980  
CCTGACATAT TCAAGTGATA GGATAAAGTT GGCCATGTAT TATGAAAAAG ATTATTTGTG 2040  
CATTTTATTG ACTGGGCAAC ACTGCAGGAC AGTCAAGGTC ATATATAATT GCTCACTGCC 2100  
TGAAAAATTA AGCACACTAA ACCAAGTTAT TTTTCTTTTT AAGAGATACT TACATTTCCA 2160  
TTTATTGTTT GAAATGTCGC GATCAAGAGA ATCAACAGAT GATAGTCCAA TTTTACTCA 2220

A

GTGATGACTG TGTAGCATTTC TCCTGTTTAC TGATTAGAGT GGTTATTTCAT TATTCCTCAG 2280  
ATTGCTGAAT CCCATCAGGC TGTATTATG AAGGAATTTG ATTGCTTTGC TGCACAGCAG 2340  
GACCTGTGCT TTGAGATTTT TTTTCTCTT TTAATATATC CTGTAACCTAC AATGATGGTA 2400  
AAGCCATGTT AAATGACTTG ATTGTACTTG GAGTAATTGC ACATTTTTTT CTATGCATAA 2460  
AAAAATGATG CAGCTGTTGA GAAAACGAAG TCTTTTTCAT TTTGCAGAAG GAAATGATGG 2520  
AATTTTTCTG TACTTCAGTA TGTGTCAACT GAGAGTCATA TACATTAGTT TTAATCTCTT 2580  
AATATTGAGA ATCAGGTTGC AAAACGGATG AGTTATTATC TATGGAAATG TGAGAAATGT 2640  
CTAATAGCCC ATAAAGTCTG AGAAATAGGT ATCAAATAG TTTAGGAAAA TGAGAGGAGA 2700  
ACAGTAGGAT TGCTGTGGCC TAGACTTCTG AGTAATTAAT AAAGAAAAAG AAGTACCAAA 2760  
AAAAAAAAAA 2770

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Val	Ser	Trp	Cys	Met	Ser	Asn	Ile	Cys	Gln	Arg	Leu	Trp	Glu	Tyr	1	5	10	15
Leu	Glu	Pro	Tyr	Leu	Pro	Cys	Leu	Ser	Thr	Glu	Ala	Asp	Lys	Ser	Thr	20	25	30	
Val	Ile	Glu	Asn	Pro	Gly	Ala	Leu	Cys	Ser	Pro	Gln	Ser	Gln	Arg	His	35	40	45	
Gly	His	Tyr	Phe	Val	Ala	Leu	Phe	Asp	Tyr	Gln	Ala	Arg	Thr	Ala	Glu	50	55	60	
Asp	Leu	Ser	Phe	Arg	Ala	Gly	Asp	Lys	Lys	Leu	Gln	Val	Leu	Asp	Thr	65	70	75	80
Leu	His	Glu	Gly	Trp	Trp	Phe	Ala	Arg	His	Leu	Glu	Lys	Arg	Arg	Asp	85	90	95	
Gly	Ser	Ser	Gln	Gln	Leu	Gln	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	100	105	110	
Glu	Asp	Arg	Ser	Leu	Gln	Ala	Glu	Pro	Trp	Phe	Phe	Gly	Ala	Ile	Gly	115	120	125	
Arg	Ser	Asp	Ala	Glu	Lys	Gln	Leu	Leu	Tyr	Ser	Glu	Asn	Lys	Thr	Gly	130	135	140	
Ser	Phe	Leu	Ile	Arg	Glu	Ser	Glu	Ser	Gln	Lys	Gly	Glu	Phe	Ser	Leu	145	150	155	160

A

Ser Val Leu Asp Gly Ala Val Val Lys His Tyr Arg Ile Lys Arg Leu  
165 170 175

Asp Glu Gly Gly Phe Phe Leu Thr Arg Arg Arg Ile Phe Ser Thr Leu  
180 185 190

Asn Glu Phe Val Ser His Tyr Thr Lys Thr Ser Asp Gly Leu Cys Val  
195 200 205

Lys Leu Gly Lys Pro Cys Leu Lys Ile Gln Val Pro Ala Pro Phe Asp  
210 215 220

Leu Ser Tyr Lys Thr Val Asp Gln Trp Glu Ile Asp Arg Asn Ser Ile  
225 230 235 240

Gln Leu Leu Lys Arg Leu Gly Ser Gly Gln Phe Gly Glu Val Trp Glu  
245 250 255

Gly Leu Trp Asn Asn Thr Thr Pro Val Ala Val Lys Thr Leu Lys Pro  
260 265 270

Gly Ser Met Asp Pro Asn Asp Phe Leu Arg Glu Ala Gln Ile Met Lys  
275 280 285

Asn Leu Arg His Pro Lys Leu Ile Gln Leu Tyr Ala Val Cys Thr Leu  
290 295 300

Glu Asp Pro Ile Tyr Ile Ile Thr Glu Leu Met Arg His Gly Ser Leu  
305 310 315 320

Gln Glu Tyr Leu Gln Asn Asp Thr Gly Ser Lys Ile His Leu Thr Gln  
325 330 335

Gln Tyr Asp Met Ala Ala Gln Val Ala Ser Gly Met Ala Tyr Leu Glu  
340 345 350

Ser Arg Asn Tyr Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu Val  
355 360 365

Gly Glu His Asn Ile Tyr Lys Val Ala Asp Phe Gly Leu Ala Arg Val  
370 375 380

Phe Lys Val Asp Asn Glu Asp Ile Tyr Glu Ser Arg His Glu Ile Lys  
385 390 395 400

Leu Pro Val Lys Trp Thr Ala Pro Glu Ala Ile Arg Ser Asn Lys Phe  
405 410 415

Ser Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Tyr Glu Ile  
420 425 430

Ile Thr Tyr Gly Lys Met Pro Tyr Ser Gly Met Thr Gly Ala Gln Val  
435 440 445

Ile Gln Met Leu Ala Gln Asn Tyr Arg Leu Pro Gln Pro Ser Asn Cys  
450 455 460

Pro Gln Gln Phe Tyr Asn Ile Met Leu Glu Cys Trp Asn Ala Glu Pro  
465 470 475 480

Lys Glu Arg Pro Thr Phe Glu Thr Leu Arg Trp Lys Leu Glu Asp Tyr  
485 490 495

A

Phe Glu Thr Asp Ser Ser Tyr Ser Asp Ala Asn Asn Phe Ile Arg  
500 505 510

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Ala	Ile	Gln	Ala	Ala	Trp	Pro	Ser	Gly	Thr	Glu	Cys	Ile	Ala	1	5	10	15
Lys	Tyr	Asn	Phe	His	Gly	Thr	Ala	Glu	Gln	Asp	Leu	Pro	Phe	Cys	Lys	20	25	30	
Gly	Asp	Val	Leu	Thr	Ile	Val	Ala	Val	Thr	Lys	Asp	Pro	Asn	Trp	Tyr	35	40	45	
Lys	Ala	Lys	Asn	Lys	Val	Gly	Arg	Glu	Gly	Ile	Ile	Pro	Ala	Asn	Tyr	50	55	60	
Val	Gln	Lys	Arg	Glu	Gly	Val	Lys	Ala	Gly	Thr	Lys	Leu	Ser	Leu	Met	65	70	75	80
Pro	Trp	Phe	His	Gly	Lys	Ile	Thr	Arg	Glu	Gln	Ala	Glu	Arg	Leu	Leu	85	90	95	
Tyr	Pro	Pro	Glu	Thr	Gly	Leu	Phe	Leu	Val	Arg	Glu	Ser	Thr	Asn	Tyr	100	105	110	
Pro	Gly	Asp	Tyr	Thr	Leu	Cys	Val	Ser	Cys	Asp	Gly	Lys	Val	Glu	His	115	120	125	
Tyr	Arg	Ile	Met	Tyr	His	Ala	Ser	Lys	Leu	Ser	Ile	Asp	Glu	Glu	Val	130	135	140	
Tyr	Phe	Glu	Asn	Leu	Met	Gln	Leu	Val	Glu	His	Tyr	Thr	Ser	Asp	Ala	145	150	155	160
Asp	Gly	Leu	Cys	Thr	Arg	Leu	Ile	Lys	Pro	Lys	Val	Met	Glu	Gly	Thr	165	170	175	
Val	Ala	Ala	Gln	Asp	Glu	Phe	Tyr	Arg	Ser	Gly	Trp	Ala	Leu	Asn	Met	180	185	190	
Lys	Glu	Leu	Lys	Leu	Leu	Gln	Thr	Ile	Gly	Lys	Gly	Glu	Phe	Gly	Asp	195	200	205	
Val	Met	Leu	Gly	Asp	Tyr	Arg	Gly	Asn	Lys	Val	Ala	Val	Lys	Cys	Ile	210	215	220	
Lys	Asn	Asp	Ala	Thr	Ala	Gln	Ala	Phe	Leu	Ala	Glu	Ala	Ser	Val	Met	225	230	235	240

KS

Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val  
 245 250 255  
 Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly  
 260 265 270  
 Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly  
 275 280 285  
 Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr  
 290 295 300  
 Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val  
 305 310 315 320  
 Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr  
 325 330 335  
 Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp  
 340 345 350  
 Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp  
 355 360 365  
 Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg  
 370 375 380  
 Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu  
 385 390 395 400  
 Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr  
 405 410 415  
 Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser  
 420 425 430  
 Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu  
 435 440 445  
 His Leu  
 450

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Ala Val Ile Leu Glu Ser Ile Phe Leu Lys Arg Ser Gln Gln  
 1 5 10 15  
 Lys Lys Lys Thr Ser Pro Leu Asn Phe Lys Lys Arg Leu Phe Leu Leu  
 20 25 30

A

Thr Val His Lys Leu Ser Tyr Tyr Glu Tyr Asp Phe Glu Arg Gly Arg  
35 40 45  
Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val  
50 55 60  
Glu Thr Val Val Pro Glu Lys Asn Pro Pro Pro Glu Arg Gln Ile Pro  
65 70 75 80  
Arg Arg Gly Glu Glu Ser Ser Glu Met Glu Gln Ile Ser Ile Ile Glu  
85 90 95  
Arg Phe Pro Tyr Pro Phe Gln Val Val Tyr Asp Glu Gly Pro Leu Tyr  
100 105 110  
Val Phe Ser Pro Thr Glu Glu Leu Arg Lys Arg Trp Ile His Gln Leu  
115 120 125  
Lys Asn Val Ile Arg Tyr Asn Ser Asp Leu Val Gln Lys Tyr His Pro  
130 135 140  
Cys Phe Trp Ile Asp Gly Gln Tyr Leu Cys Cys Ser Gln Thr Ala Lys  
145 150 155 160  
Asn Ala Met Gly Cys Gln Ile Leu Glu Asn Arg Asn Gly Ser Leu Lys  
165 170 175  
Pro Gly Ser Ser His Arg Lys Thr Lys Lys Pro Leu Pro Pro Thr Pro  
180 185 190  
Glu Glu Asp Gln Ile Leu Lys Lys Pro Leu Pro Pro Glu Pro Ala Ala  
195 200 205  
Ala Pro Val Ser Thr Ser Glu Leu Lys Lys Val Val Ala Leu Tyr Asp  
210 215 220  
Tyr Met Pro Met Asn Ala Asn Asp Leu Gln Leu Arg Lys Gly Asp Glu  
225 230 235 240  
Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Trp Trp Arg Ala Arg Asp  
245 250 255  
Lys Asn Gly Gln Glu Gly Tyr Ile Pro Ser Asn Tyr Val Thr Glu Ala  
260 265 270  
Glu Asp Ser Ile Glu Met Tyr Glu Trp Tyr Ser Lys His Met Thr Arg  
275 280 285  
Ser Gln Ala Glu Gln Leu Leu Lys Gln Glu Gly Lys Glu Gly Gly Phe  
290 295 300  
Ile Val Arg Asp Ser Ser Lys Ala Gly Lys Tyr Thr Val Ser Val Phe  
305 310 315 320  
Ala Lys Ser Thr Gly Asp Pro Gln Gly Val Ile Arg His Tyr Val Val  
325 330 335  
Cys Ser Thr Pro Gln Ser Gln Tyr Tyr Leu Ala Glu Lys His Leu Phe  
340 345 350  
Ser Thr Ile Pro Glu Leu Ile Asn Tyr His Gln His Asn Ser Ala Gly  
355 360 365

A

Leu Ile Ser Arg Leu Lys Tyr Pro Val Ser Gln Gln Asn Lys Asn Ala  
 370 375 380  
 Pro Ser Thr Ala Gly Leu Gly Tyr Gly Ser Trp Glu Ile Asp Pro Lys  
 385 390 395 400  
 Asp Leu Thr Phe Leu Lys Glu Leu Gly Thr Gly Gln Phe Gly Val Val  
 405 410 415  
 Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala Ile Lys Met Ile  
 420 425 430  
 Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu Glu Ala Lys Val  
 435 440 445  
 Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu Tyr Gly Val Cys  
 450 455 460  
 Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr Met Ala Asn Gly  
 465 470 475 480  
 Cys Leu Leu Asn Tyr Leu Arg Glu Met Arg His Arg Phe Gln Thr Gln  
 485 490 495  
 Gln Leu Leu Glu Met Cys Lys Asp Val Cys Glu Ala Met Glu Tyr Leu  
 500 505 510  
 Glu Ser Lys Gln Phe Leu His Arg Asp Leu Ala Ala Arg Asn Cys Leu  
 515 520 525  
 Val Asn Asp Gln Gly Val Val Lys Val Ser Asp Phe Gly Leu Ser Arg  
 530 535 540  
 Tyr Val Leu Asp Asp Glu Tyr Thr Ser Ser Val Gly Ser Lys Phe Pro  
 545 550 555 560  
 Val Arg Trp Ser Pro Pro Glu Val Leu Met Tyr Ser Lys Phe Ser Ser  
 565 570 575  
 Lys Ser Asp Ile Trp Ala Phe Gly Val Leu Met Trp Glu Ile Tyr Ser  
 580 585 590  
 Leu Gly Lys Met Pro Tyr Glu Arg Phe Thr Asn Ser Glu Thr Ala Glu  
 595 600 605  
 His Ile Ala Gln Gly Leu Arg Leu Tyr Arg Pro His Leu Ala Ser Glu  
 610 615 620  
 Lys Val Tyr Thr Ile Met Tyr Ser Cys Trp His Glu Lys Ala Asp Glu  
 625 630 635 640  
 Arg Pro Thr Phe Lys Ile Leu Leu Ser Asn Ile Leu Asp Val Met Asp  
 645 650 655  
 Glu Glu Ser

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 620 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown

A

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Asn	Asn	Phe	Ile	Leu	Leu	Glu	Glu	Gln	Leu	Ile	Lys	Lys	Ser	Gln
1				5					10					15	
Gln	Lys	Arg	Arg	Thr	Ser	Pro	Ser	Asn	Phe	Lys	Val	Arg	Phe	Phe	Val
			20					25					30		
Leu	Thr	Lys	Ala	Ser	Leu	Ala	Tyr	Phe	Glu	Asp	Arg	His	Gly	Lys	Lys
		35					40					45			
Arg	Thr	Leu	Lys	Gly	Ser	Ile	Glu	Leu	Ser	Arg	Ile	Lys	Cys	Val	Glu
	50					55					60				
Ile	Val	Lys	Ser	Asp	Ile	Ser	Ile	Pro	Cys	His	Tyr	Lys	Tyr	Pro	Phe
65					70					75					80
Gln	Val	Val	His	Asp	Asn	Tyr	Leu	Leu	Tyr	Val	Phe	Ala	Pro	Asp	Arg
				85					90					95	
Glu	Ser	Arg	Gln	Arg	Trp	Val	Leu	Ala	Leu	Lys	Glu	Glu	Thr	Arg	Asn
			100				105						110		
Asn	Asn	Ser	Leu	Val	Pro	Lys	Tyr	His	Pro	Asn	Phe	Trp	Met	Asp	Gly
		115					120					125			
Lys	Trp	Arg	Cys	Cys	Ser	Gln	Leu	Glu	Lys	Leu	Ala	Thr	Gly	Cys	Ala
	130					135					140				
Gln	Tyr	Asp	Pro	Thr	Lys	Asn	Ala	Ser	Lys	Lys	Pro	Leu	Pro	Pro	Thr
145					150					155					160
Pro	Glu	Asp	Asn	Arg	Arg	Pro	Leu	Trp	Glu	Pro	Glu	Glu	Thr	Val	Val
				165					170					175	
Ile	Ala	Leu	Tyr	Asp	Tyr	Gln	Thr	Asn	Asp	Pro	Gln	Glu	Leu	Ala	Leu
			180					185					190		
Arg	Arg	Asn	Glu	Glu	Tyr	Cys	Leu	Leu	Asp	Ser	Ser	Glu	Ile	His	Trp
		195					200					205			
Trp	Arg	Val	Gln	Asp	Arg	Asn	Gly	His	Glu	Gly	Tyr	Val	Pro	Ser	Ser
	210					215					220				
Tyr	Leu	Val	Glu	Lys	Ser	Pro	Asn	Asn	Leu	Glu	Thr	Tyr	Glu	Trp	Tyr
225					230					235					240
Asn	Lys	Ser	Ile	Ser	Arg	Asp	Lys	Ala	Glu	Lys	Leu	Leu	Leu	Asp	Thr
				245					250					255	
Gly	Lys	Glu	Gly	Ala	Phe	Met	Val	Arg	Asp	Ser	Arg	Thr	Ala	Gly	Thr
			260					265					270		
Tyr	Thr	Val	Ser	Val	Phe	Thr	Lys	Ala	Val	Val	Ser	Glu	Asn	Asn	Pro
		275					280					285			
Cys	Ile	Lys	His	Tyr	His	Ile	Lys	Glu	Thr	Asn	Asp	Asn	Pro	Lys	Arg

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290						295						300					
Tyr	Tyr	Val	Ala	Glu	Lys	Tyr	Val	Phe	Asp	Ser	Ile	Pro	Leu	Leu	Ile		
305					310					315					320		
Asn	Tyr	His	Gln	His	Asn	Gly	Gly	Gly	Leu	Val	Thr	Arg	Leu	Arg	Tyr		
				325					330					335			
Pro	Val	Cys	Phe	Gly	Arg	Gln	Lys	Ala	Pro	Val	Thr	Ala	Gly	Leu	Arg		
			340					345					350				
Tyr	Gly	Lys	Trp	Val	Ile	Asp	Pro	Ser	Glu	Leu	Thr	Phe	Val	Gln	Glu		
		355					360					365					
Ile	Gly	Ser	Gly	Gln	Phe	Gly	Leu	Val	His	Leu	Gly	Tyr	Trp	Leu	Asn		
	370					375					380						
Lys	Asp	Lys	Val	Ala	Ile	Lys	Thr	Ile	Arg	Glu	Gly	Ala	Met	Ser	Glu		
385					390					395					400		
Glu	Asp	Phe	Ile	Glu	Glu	Ala	Glu	Val	Met	Met	Lys	Leu	Ser	His	Pro		
				405					410					415			
Lys	Leu	Val	Gln	Leu	Tyr	Gly	Val	Cys	Leu	Glu	Gln	Ala	Pro	Ile	Cys		
			420					425					430				
Leu	Val	Phe	Glu	Phe	Met	Glu	His	Gly	Cys	Leu	Ser	Asp	Tyr	Leu	Arg		
		435					440					445					
Thr	Gln	Arg	Gly	Leu	Phe	Ala	Ala	Glu	Thr	Leu	Leu	Gly	Met	Cys	Leu		
	450					455					460						
Asp	Val	Cys	Glu	Gly	Met	Ala	Tyr	Leu	Glu	Glu	Ala	Cys	Val	Ile	His		
465					470				475					480			
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Leu	Val	Gly	Glu	Asn	Gln	Val	Ile		
				485					490					495			
Lys	Val	Ser	Asp	Phe	Gly	Met	Thr	Arg	Phe	Val	Leu	Asp	Asp	Gln	Tyr		
			500					505					510				
Thr	Ser	Ser	Thr	Gly	Thr	Lys	Phe	Pro	Val	Lys	Trp	Ala	Ser	Pro	Glu		
		515					520					525					
Val	Phe	Ser	Phe	Ser	Arg	Tyr	Ser	Ser	Lys	Ser	Asp	Val	Trp	Ser	Phe		
	530					535					540						
Gly	Val	Leu	Met	Trp	Glu	Val	Phe	Ser	Glu	Gly	Lys	Ile	Pro	Tyr	Glu		
545					550					555					560		
Asn	Arg	Ser	Asn	Ser	Glu	Val	Val	Glu	Asp	Ile	Ser	Thr	Gly	Phe	Arg		
				565					570					575			
Leu	Tyr	Lys	Pro	Arg	Leu	Ala	Ser	Thr	His	Val	Tyr	Gln	Ile	Met	Asn		
			580					585					590				
His	Cys	Trp	Lys	Glu	Arg	Pro	Glu	Asp	Arg	Pro	Ala	Phe	Ser	Arg	Leu		
		595					600					605					
Leu	Arg	Gln	Leu	Ala	Glu	Ile	Ala	Glu	Ser	Gly	Leu						
	610					615					620						

(2) INFORMATION FOR SEQ ID NO:10:

19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Met	Val	Ser	Phe	Pro	Val	Lys	Ile	Asn	Phe	His	Ser	Ser	Pro	Gln
1				5					10					15	
Ser	Arg	Asp	Arg	Trp	Val	Lys	Lys	Leu	Lys	Glu	Glu	Ile	Lys	Asn	Asn
		20						25					30		
Asn	Asn	Ile	Met	Ile	Lys	Tyr	His	Pro	Lys	Phe	Trp	Ala	Asp	Gly	Ser
		35					40					45			
Tyr	Gln	Cys	Cys	Arg	Gln	Thr	Glu	Lys	Leu	Ala	Pro	Gly	Cys	Glu	Lys
	50					55					60				
Tyr	Asn	Leu	Phe	Glu	Ser	Ser	Ile	Arg	Lys	Thr	Leu	Pro	Pro	Ala	Pro
65					70					75					80
Glu	Ile	Lys	Lys	Arg	Arg	Pro	Pro	Pro	Ile	Pro	Pro	Glu	Glu	Glu	
				85				90					95		
Asn	Thr	Glu	Glu	Ile	Val	Val	Ala	Met	Tyr	Asp	Phe	Gln	Ala	Thr	Glu
			100					105					110		
Ala	His	Asp	Leu	Arg	Leu	Glu	Arg	Gly	Gln	Glu	Tyr	Ile	Ile	Leu	Glu
		115					120					125			
Lys	Asn	Asp	Leu	His	Trp	Trp	Arg	Ala	Arg	Asp	Lys	Tyr	Gly	Trp	Tyr
	130					135					140				
Cys	Arg	Asn	Thr	Asn	Arg	Ser	Lys	Ala	Glu	Gln	Leu	Leu	Arg	Thr	Glu
145					150					155					160
Asp	Lys	Glu	Gly	Gly	Phe	Met	Val	Arg	Asp	Ser	Ser	Gln	Pro	Gly	Leu
				165					170					175	
Tyr	Thr	Val	Ser	Leu	Tyr	Thr	Lys	Phe	Gly	Gly	Glu	Gly	Ser	Ser	Gly
			180					185					190		
Phe	Arg	His	Tyr	His	Ile	Lys	Glu	Thr	Ala	Thr	Ser	Pro	Lys	Lys	Tyr
		195					200					205			
Tyr	Leu	Ala	Glu	Lys	His	Ala	Phe	Gly	Ser	Ile	Pro	Glu	Ile	Ile	Glu
	210					215					220				
Tyr	His	Lys	His	Asn	Ala	Ala	Gly	Leu	Val	Thr	Arg	Leu	Arg	Tyr	Pro
225					230					235					240
Val	Ser	Thr	Lys	Gly	Lys	Asn	Ala	Pro	Thr	Thr	Ala	Gly	Phe	Ser	Tyr
				245					250				255		
Asp	Lys	Trp	Glu	Ile	Asn	Pro	Ser	Glu	Leu	Thr	Phe	Met	Arg	Glu	Leu
			260					265					270		

Gly Ser Gly Leu Phe Gly Val Val Arg Leu Gly Lys Trp Arg Ala Gln  
 275 280 285  
 Tyr Lys Val Ala Ile Lys Ala Ile Arg Glu Gly Ala Met Cys Glu Glu  
 290 295 300  
 Asp Phe Ile Glu Glu Ala Lys Val Met Met Lys Leu Thr His Pro Lys  
 305 310 315 320  
 Leu Val Gln Leu Tyr Gly Val Cys Thr Gln Gln Lys Pro Ile Tyr Ile  
 325 330 335  
 Val Thr Glu Phe Met Glu Arg Gly Cys Leu Leu Asn Phe Leu Arg Gln  
 340 345 350  
 Arg Gln Gly His Phe Ser Arg Asp Met Leu Leu Ser Met Cys Gln Asp  
 355 360 365  
 Val Cys Glu Gly Met Glu Tyr Leu Glu Arg Asn Ser Phe Ile His Arg  
 370 375 380  
 Asp Leu Ala Ala Arg Asn Cys Leu Val Asn Glu Ala Gly Val Val Lys  
 385 390 395 400  
 Val Ser Asp Phe Gly Met Ala Arg Tyr Val Leu Asp Asp Gln Tyr Thr  
 405 410 415  
 Ser Ser Ser Gly Ala Lys Phe Pro Val Lys Trp Cys Pro Pro Glu Val  
 420 425 430  
 Phe Asn Tyr Ser Arg Phe Ser Ser Lys Ser Asp Val Trp Ser Phe Gly  
 435 440 445  
 Val Leu Met Trp Glu Ile Phe Thr Glu Gly Arg Met Pro Phe Glu Lys  
 450 455 460  
 Asn Thr Asn Tyr Glu Val Val Thr Met Val Thr Arg Gly His Arg Leu  
 465 470 475 480  
 His Arg Pro Lys Leu Ala Thr Lys Tyr Leu Tyr Glu Val Met Leu Arg  
 485 490 495  
 Cys Trp Gln Glu Arg Pro Glu Gly Arg Pro Ser Phe Glu Asp Leu Leu  
 500 505 510  
 Arg Thr Ile Asp Glu Leu Val Glu Cys Glu Glu Thr Phe Gly Arg  
 515 520 525

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu  
1 5 10 15  
Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr  
20 25 30  
Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro  
35 40 45  
Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe  
50 55 60  
Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly  
65 70 75 80  
Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg  
85 90 95  
Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu  
100 105 110  
Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly  
115 120 125  
Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile  
130 135 140  
Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu  
145 150 155 160  
Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg  
165 170 175  
Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp  
180 185 190  
Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu  
195 200 205  
Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu  
210 215 220  
Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys  
225 230 235 240  
Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu  
245 250 255  
Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln  
260 265 270  
Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly  
275 280 285  
Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly  
290 295 300  
Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys  
305 310 315 320

Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu  
 325 330 335  
 Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp  
 340 345 350  
 Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val  
 355 360 365  
 Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met  
 370 375 380  
 Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn  
 385 390 395 400  
 Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu  
 405 410 415  
 Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp  
 420 425 430  
 Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp  
 435 440 445  
 Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg  
 450 455 460  
 Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu  
 465 470 475 480  
 Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His  
 485 490 495  
 Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr  
 500 505 510  
 Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu  
 515 520 525  
 Pro Gln Tyr Gln Pro Gly Glu Asn Leu  
 530 535

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly  
 1 5 10 15  
 Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro  
 20 25 30

8

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn  
35 40 45  
Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro  
50 55 60  
Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly  
65 70 75 80  
Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr  
85 90 95  
Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn  
100 105 110  
Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala  
115 120 125  
Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln  
130 135 140  
Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg  
145 150 155 160  
Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu  
165 170 175  
Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp  
180 185 190  
Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp  
195 200 205  
Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln  
210 215 220  
Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg  
225 230 235 240  
Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser  
245 250 255  
Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu  
260 265 270  
Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr  
275 280 285  
Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr  
290 295 300  
Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu  
305 310 315 320  
Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro  
325 330 335  
Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe  
340 345 350  
Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp  
355 360 365

18

Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn  
 370 375 380  
 Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn  
 385 390 395 400  
 Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp  
 405 410 415  
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr  
 420 425 430  
 Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val  
 435 440 445  
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val  
 450 455 460  
 Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg  
 465 470 475 480  
 Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp  
 485 490 495  
 Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe  
 500 505 510  
 Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro  
 515 520 525  
 Gln Tyr Gln Pro Gly Asp Asn Gln  
 530 535

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg  
 1 5 10 15  
 Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe  
 20 25 30  
 Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg  
 35 40 45  
 Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe  
 50 55 60  
 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly  
 65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu  
85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln  
100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser  
115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp  
130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu  
145 150 155 160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu  
165 170 175

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser  
180 185 190

Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg  
195 200 205

Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn  
210 215 220

Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu  
225 230 235 240

Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln  
245 250 255

Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu  
260 265 270

Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr  
275 280 285

Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr  
290 295 300

Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu  
305 310 315 320

Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro  
325 330 335

Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe  
340 345 350

Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp  
355 360 365

Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn  
370 375 380

Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn  
385 390 395 400

Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp  
405 410 415



Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr  
 420 425 430  
 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val  
 435 440 445  
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val  
 450 455 460  
 Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg  
 465 470 475 480  
 Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp  
 485 490 495  
 Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe  
 500 505 510  
 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro  
 515 520 525  
 Gln Tyr Gln Pro Gly Glu Asn Leu  
 530 535

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr  
 1 5 10 15  
 Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr  
 20 25 30  
 Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ala Lys  
 35 40 45  
 Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly  
 50 55 60  
 Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val  
 65 70 75 80  
 Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe  
 85 90 95  
 Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe  
 100 105 110  
 Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp  
 115 120 125  
 Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser

A

130					135					140						
Asn	Tyr	Val	Ala	Pro	Ala	Asp	Ser	Ile	Gln	Ala	Glu	Glu	Trp	Tyr	Phe	
145					150					155					160	
Gly	Lys	Met	Gly	Arg	Lys	Asp	Ala	Glu	Arg	Leu	Leu	Leu	Asn	Pro	Gly	
				165					170					175		
Asn	Gln	Arg	Gly	Ile	Phe	Leu	Val	Arg	Glu	Ser	Glu	Thr	Thr	Lys	Gly	
			180					185					190			
Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp	Glu	Ile	Arg	Gly	Asp	Asn	
		195				200						205				
Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	Asn	Gly	Gly	Tyr	Tyr	Ile	
	210					215					220					
Thr	Thr	Arg	Ala	Gln	Phe	Asp	Thr	Leu	Gln	Lys	Leu	Val	Lys	His	Tyr	
225					230					235					240	
Thr	Glu	His	Ala	Asp	Gly	Leu	Cys	His	Lys	Leu	Thr	Thr	Val	Cys	Pro	
				245					250					255		
Thr	Val	Lys	Pro	Gln	Thr	Gln	Gly	Leu	Ala	Lys	Asp	Ala	Trp	Glu	Ile	
			260				265						270			
Pro	Arg	Glu	Ser	Leu	Arg	Leu	Glu	Val	Lys	Leu	Gly	Gln	Gly	Cys	Phe	
		275					280					285				
Gly	Glu	Val	Trp	Met	Gly	Thr	Trp	Asn	Gly	Thr	Thr	Lys	Val	Ala	Ile	
	290					295					300					
Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Met	Pro	Glu	Ala	Phe	Leu	Gln	Glu	
305					310					315					320	
Ala	Gln	Ile	Met	Lys	Lys	Leu	Arg	His	Asp	Lys	Leu	Val	Pro	Leu	Tyr	
				325					330					335		
Ala	Val	Val	Ser	Glu	Glu	Pro	Ile	Tyr	Ile	Val	Thr	Glu	Phe	Met	Ser	
			340					345					350			
Lys	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Glu	Gly	Asp	Gly	Lys	Tyr	Leu	
		355					360					365				
Lys	Leu	Pro	Gln	Leu	Val	Asp	Met	Ala	Ala	Gln	Ile	Ala	Asp	Gly	Met	
	370					375					380					
Ala	Tyr	Ile	Glu	Arg	Met	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	Ala	Ala	
385					390					395					400	
Asn	Ile	Leu	Val	Gly	Glu	Asn	Leu	Val	Cys	Lys	Ile	Ala	Asp	Phe	Gly	
				405					410					415		
Leu	Ala	Arg	Leu	Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	Arg	Gln	Gly	Ala	
			420					425					430			
Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ala	Leu	Tyr	Gly	Arg	
		435					440					445				
Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Gln	Thr	Glu	
450						455					460					

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu  
465 470 475 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly  
485 490 495

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp  
500 505 510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp  
515 520 525

Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu  
530 535 540

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 529 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys  
1 5 10 15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp  
20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala  
35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly  
50 55 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr  
65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu  
85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly  
100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile  
115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp  
130 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser  
145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr  
165 170 175

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Lys	Gly	Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp	Gln	Thr	Arg	Gly		
			180					185					190				
Asp	His	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	Met	Gly	Gly	Tyr		
		195					200					205					
Tyr	Ile	Thr	Thr	Arg	Val	Gln	Phe	Asn	Ser	Val	Gln	Glu	Leu	Val	Gln		
	210					215					220						
His	Tyr	Met	Glu	Val	Asn	Asp	Gly	Leu	Cys	Asn	Leu	Leu	Ile	Ala	Pro		
225					230					235					240		
Cys	Thr	Ile	Met	Lys	Pro	Gln	Thr	Leu	Gly	Leu	Ala	Lys	Asp	Ala	Trp		
				245					250					255			
Glu	Ile	Ser	Arg	Ser	Ser	Ile	Thr	Leu	Glu	Arg	Arg	Leu	Gly	Thr	Gly		
			260					265					270				
Cys	Phe	Gly	Asp	Val	Trp	Leu	Gly	Thr	Trp	Asn	Gly	Ser	Thr	Lys	Val		
		275					280					285					
Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Ser	Pro	Lys	Ala	Phe	Leu		
	290					295					300						
Glu	Glu	Ala	Gln	Val	Met	Lys	Leu	Leu	Arg	His	Asp	Lys	Leu	Val	Gln		
305					310					315					320		
Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu	Pro	Ile	Tyr	Ile	Val	Thr	Glu	Phe		
				325					330					335			
Met	Cys	His	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Asn	Pro	Glu	Gly	Gln		
			340					345					350				
Asp	Leu	Arg	Leu	Pro	Gln	Leu	Val	Asp	Met	Ala	Ala	Gln	Val	Ala	Glu		
		355					360					365					
Gly	Met	Ala	Tyr	Met	Glu	Arg	Met	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg		
	370					375					380						
Ala	Ala	Asn	Ile	Leu	Val	Gly	Glu	Arg	Leu	Ala	Cys	Lys	Ile	Ala	Asp		
385					390					395					400		
Phe	Gly	Leu	Ala	Arg	Leu	Ile	Lys	Asp	Asp	Glu	Tyr	Asn	Pro	Cys	Gln		
				405					410					415			
Gly	Ser	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ala	Leu	Phe		
			420					425					430				
Gly	Arg	Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Leu		
		435					440					445					
Thr	Glu	Leu	Ile	Thr	Lys	Gly	Arg	Ile	Pro	Tyr	Pro	Gly	Met	Asn	Lys		
	450					455					460						
Arg	Glu	Val	Leu	Glu	Gln	Val	Glu	Gln	Gly	Tyr	His	Met	Pro	Cys	Pro		
465					470					475					480		
Pro	Gly	Cys	Pro	Ala	Ser	Leu	Tyr	Glu	Ala	Met	Glu	Gln	Thr	Trp	Arg		
				485					490					495			
Leu	Asp	Pro	Glu	Glu	Arg	Pro	Thr	Phe	Glu	Tyr	Leu	Gln	Ser	Phe	Leu		
			500					505					510				

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Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln  
515 520 525

Thr

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly  
1 5 10 15  
Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr  
20 25 30  
Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser  
35 40 45  
Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln  
50 55 60  
Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp  
65 70 75 80  
Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His  
85 90 95  
Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe  
100 105 110  
Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu  
115 120 125  
Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu  
130 135 140  
Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr  
145 150 155 160  
Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His  
165 170 175  
Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly  
180 185 190  
Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile  
195 200 205  
Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys  
210 215 220

Ala	Cys	Ile	Ser	Pro	Lys	Pro	Gln	Lys	Pro	Trp	Asp	Lys	Asp	Ala	Trp
225					230					235					240
Glu	Ile	Pro	Arg	Glu	Ser	Ile	Lys	Leu	Val	Lys	Arg	Leu	Gly	Ala	Gly
				245					250					255	
Gln	Phe	Gly	Glu	Val	Trp	Met	Gly	Tyr	Tyr	Asn	Asn	Ser	Thr	Lys	Val
			260					265					270		
Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Ser	Val	Gln	Ala	Phe	Leu
		275					280					285			
Glu	Glu	Ala	Asn	Leu	Met	Lys	Thr	Leu	Gln	His	Asp	Lys	Leu	Val	Arg
	290					295					300				
Leu	Tyr	Ala	Val	Val	Thr	Arg	Glu	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu
305					310					315					320
Tyr	Met	Ala	Lys	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Ser	Asp	Glu	Gly
				325					330					335	
Gly	Lys	Val	Leu	Leu	Pro	Lys	Leu	Ile	Asp	Phe	Ser	Ala	Gln	Ile	Ala
			340					345					350		
Glu	Gly	Met	Ala	Tyr	Ile	Glu	Arg	Lys	Asn	Tyr	Ile	His	Arg	Asp	Leu
		355					360					365			
Arg	Ala	Ala	Asn	Val	Leu	Val	Ser	Glu	Ser	Leu	Met	Cys	Lys	Ile	Ala
	370					375					380				
Asp	Phe	Gly	Leu	Ala	Arg	Val	Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	Arg
385					390					395					400
Glu	Gly	Ala	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Asn
				405					410					415	
Phe	Gly	Cys	Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu
			420					425					430		
Leu	Tyr	Glu	Ile	Val	Thr	Tyr	Gly	Lys	Ile	Pro	Tyr	Pro	Gly	Arg	Thr
		435					440					445			
Asn	Ala	Asp	Val	Met	Thr	Ala	Leu	Ser	Gln	Gly	Tyr	Arg	Met	Pro	Arg
	450					455					460				
Val	Glu	Asn	Cys	Pro	Asp	Glu	Leu	Tyr	Asp	Ile	Met	Lys	Met	Cys	Trp
465					470					475					480
Lys	Glu	Lys	Ala	Glu	Glu	Arg	Pro	Thr	Phe	Asp	Tyr	Leu	Gln	Ser	Val
				485					490					495	
Leu	Asp	Asp	Phe	Tyr	Thr	Ala	Thr	Glu	Gly	Gln	Tyr	Gln	Gln	Gln	Pro
			500					505					510		

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Gly	Ser	Met	Lys	Ser	Lys	Phe	Leu	Gln	Val	Gly	Gly	Asn	Thr	Phe	
1				5					10					15		
Ser	Lys	Thr	Glu	Thr	Ser	Ala	Ser	Pro	His	Cys	Pro	Val	Tyr	Val	Pro	
			20					25					30			
Asp	Pro	Thr	Ser	Thr	Ile	Lys	Pro	Gly	Pro	Asn	Ser	His	Asn	Ser	Asn	
			35				40					45				
Thr	Pro	Gly	Ile	Arg	Glu	Ala	Gly	Ser	Glu	Asp	Ile	Ile	Val	Val	Ala	
	50					55					60					
Leu	Tyr	Asp	Tyr	Glu	Ala	Ile	His	His	Glu	Asp	Leu	Ser	Phe	Gln	Lys	
65					70					75					80	
Gly	Asp	Gln	Met	Val	Val	Leu	Glu	Glu	Ser	Gly	Glu	Trp	Trp	Lys	Ala	
				85					90					95		
Arg	Ser	Leu	Ala	Thr	Arg	Lys	Glu	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	
			100				105						110			
Ala	Arg	Val	Asp	Ser	Leu	Glu	Thr	Glu	Glu	Trp	Phe	Phe	Lys	Gly	Ile	
		115					120					125				
Ser	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu	Ala	Pro	Gly	Asn	Met	Leu	
	130					135					140					
Gly	Ser	Phe	Met	Ile	Arg	Asp	Ser	Glu	Thr	Thr	Lys	Gly	Ser	Tyr	Ser	
145					150					155					160	
Leu	Ser	Val	Arg	Asp	Tyr	Asp	Pro	Arg	Gln	Gly	Asp	Thr	Val	Lys	His	
				165					170					175		
Tyr	Lys	Ile	Arg	Thr	Leu	Asp	Asn	Gly	Gly	Phe	Tyr	Ile	Ser	Pro	Arg	
			180				185						190			
Ser	Thr	Phe	Ser	Thr	Leu	Gln	Glu	Leu	Val	Asp	His	Tyr	Lys	Lys	Gly	
		195					200					205				
Asn	Asp	Gly	Leu	Cys	Gln	Lys	Leu	Ser	Val	Pro	Cys	Met	Ser	Ser	Lys	
	210					215					220					
Pro	Gln	Lys	Pro	Trp	Glu	Lys	Asp	Ala	Trp	Glu	Ile	Pro	Arg	Glu	Ser	
225					230					235					240	
Leu	Lys	Leu	Glu	Lys	Lys	Leu	Gly	Ala	Gly	Gln	Phe	Gly	Glu	Val	Trp	
				245					250					255		
Met	Ala	Thr	Tyr	Asn	Lys	His	Thr	Lys	Val	Ala	Val	Lys	Thr	Met	Lys	
			260					265					270			
Pro	Gly	Ser	Met	Ser	Val	Glu	Ala	Phe	Leu	Ala	Glu	Ala	Asn	Val	Met	
		275					280					285				
Lys	Thr	Leu	Gln	His	Asp	Lys	Leu	Val	Lys	Leu	His	Ala	Val	Val	Thr	
	290					295					300					

Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala Lys Gly Ser Leu  
 305 310 315 320  
 Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys  
 325 330 335  
 Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu  
 340 345 350  
 Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val  
 355 360 365  
 Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val  
 370 375 380  
 Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile  
 385 390 395 400  
 Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys  
 405 410 415  
 Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr  
 420 425 430  
 Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala  
 435 440 445  
 Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu  
 450 455 460  
 Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg  
 465 470 475 480  
 Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala  
 485 490 495  
 Thr Glu Ser Gln Tyr Gln Gln Gln Pro  
 500 505

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn  
 1 5 10 15  
 Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly  
 20 25 30  
 Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu  
 35 40 45

8



Val	Thr	Tyr	Glu	Gly	Ser	Asn	Pro	Pro	Ala	Ser	Pro	Leu	Gln	Asp	Asn	
50						55					60					
Leu	Val	Ile	Ala	Leu	His	Ser	Tyr	Glu	Pro	Ser	His	Asp	Gly	Asp	Leu	
65					70					75					80	
Gly	Phe	Glu	Lys	Gly	Glu	Gln	Leu	Arg	Ile	Leu	Glu	Gln	Ser	Gly	Glu	
				85					90					95		
Trp	Trp	Lys	Ala	Gln	Ser	Leu	Thr	Thr	Gly	Gln	Glu	Gly	Phe	Ile	Pro	
			100					105					110			
Phe	Asn	Phe	Val	Ala	Lys	Ala	Asn	Ser	Leu	Glu	Pro	Glu	Pro	Trp	Phe	
			115				120					125				
Phe	Lys	Asn	Leu	Ser	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu	Ala	Pro	
			130			135					140					
Gly	Asn	Thr	His	Gly	Ser	Phe	Leu	Ile	Arg	Glu	Ser	Glu	Ser	Thr	Ala	
145					150					155					160	
Gly	Ser	Phe	Ser	Leu	Ser	Val	Arg	Asp	Phe	Asp	Gln	Asn	Gln	Gly	Glu	
				165					170					175		
Val	Val	Lys	His	Tyr	Lys	Ile	Arg	Asn	Leu	Asp	Asn	Gly	Gly	Phe	Tyr	
			180				185						190			
Ile	Ser	Pro	Arg	Ile	Thr	Phe	Pro	Gly	Leu	His	Glu	Leu	Val	Arg	His	
		195					200					205				
Tyr	Thr	Asn	Ala	Ser	Asp	Gly	Leu	Cys	Thr	Arg	Leu	Ser	Arg	Pro	Cys	
	210					215					220					
Gln	Thr	Gln	Lys	Pro	Gln	Lys	Pro	Trp	Trp	Glu	Asp	Glu	Trp	Glu	Val	
225					230					235					240	
Pro	Arg	Glu	Thr	Leu	Lys	Leu	Val	Glu	Arg	Leu	Gly	Ala	Gly	Gln	Phe	
				245					250					255		
Gly	Glu	Val	Trp	Met	Gly	Tyr	Tyr	Asn	Gly	His	Thr	Lys	Val	Ala	Val	
			260					265					270			
Lys	Ser	Leu	Lys	Gln	Gly	Ser	Met	Ser	Pro	Asp	Ala	Phe	Leu	Ala	Glu	
		275					280					285				
Ala	Asn	Leu	Met	Lys	Gln	Leu	Gln	His	Gln	Arg	Leu	Val	Arg	Leu	Tyr	
	290					295					300					
Ala	Val	Val	Thr	Gln	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Tyr	Met	Glu	
305					310					315					320	
Asn	Gly	Ser	Leu	Val	Asp	Phe	Leu	Lys	Thr	Pro	Ser	Gly	Ile	Lys	Leu	
				325					330					335		
Thr	Ile	Asn	Lys	Leu	Leu	Asp	Met	Ala	Ala	Gln	Ile	Ala	Glu	Gly	Met	
		340						345					350			
Ala	Phe	Ile	Glu	Glu	Arg	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	Ala	Ala	
		355					360					365				
Asn	Ile	Leu	Val	Ser	Asp	Thr	Leu	Ser	Cys	Lys	Ile	Ala	Asp	Phe	Gly	
	370					375					380					

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala  
385 390 395 400

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr  
405 410 415

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu  
420 425 430

Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu  
435 440 445

Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn  
450 455 460

Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg  
465 470 475 480

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp  
485 490 495

Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro  
500 505

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 499 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gly Leu Leu Ser Ser Lys Arg Gln Val Ser Glu Lys Gly Lys Gly  
1 5 10 15

Trp Ser Pro Val Lys Ile Arg Thr Gln Asp Lys Ala Pro Pro Pro Leu  
20 25 30

Pro Pro Leu Val Val Phe Asn His Leu Ala Pro Pro Ser Pro Asn Gln  
35 40 45

Asp Pro Asp Glu Glu Glu Arg Phe Val Val Ala Leu Phe Asp Tyr Ala  
50 55 60

Ala Val Asn Asp Arg Asp Leu Gln Val Leu Lys Gly Glu Lys Leu Gln  
65 70 75 80

Val Leu Arg Ser Thr Gly Asp Trp Trp Leu Ala Arg Ser Leu Val Thr  
85 90 95

Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe Val Ala Pro Val Glu Thr  
100 105 110

Leu Glu Val Glu Lys Trp Phe Phe Arg Thr Ile Ser Arg Lys Asp Ala  
115 120 125

8

Glu Arg Gln Leu Leu Ala Pro Met Asn Lys Ala Gly Ser Phe Leu Ile  
130 135 140  
Arg Glu Ser Glu Ser Asn Lys Gly Ala Phe Ser Leu Ser Val Lys Asp  
145 150 155 160  
Ile Thr Thr Gln Gly Glu Val Val Lys His Tyr Lys Ile Arg Ser Leu  
165 170 175  
Asp Asn Gly Gly Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Thr Leu  
180 185 190  
Gln Ala Leu Val Gln His Tyr Ser Lys Lys Gly Asp Gly Leu Cys Gln  
195 200 205  
Lys Leu Thr Leu Pro Cys Val Asn Leu Ala Pro Lys Asn Leu Trp Ala  
210 215 220  
Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser Leu Lys Leu Val Arg Lys  
225 230 235 240  
Leu Gly Ser Gly Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Lys Asn  
245 250 255  
Asn Met Lys Val Ala Ile Lys Thr Leu Lys Glu Gly Thr Met Ser Pro  
260 265 270  
Glu Ala Phe Leu Gly Glu Ala Asn Val Met Lys Thr Leu Gln His Glu  
275 280 285  
Arg Leu Val Arg Leu Tyr Ala Val Val Thr Arg Glu Pro Ile Tyr Ile  
290 295 300  
Val Thr Glu Tyr Met Ala Arg Gly Cys Leu Leu Asp Phe Leu Lys Thr  
305 310 315 320  
Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg Leu Ile Asp Met Ser Ala  
325 330 335  
Gln Val Ala Glu Gly Met Ala Tyr Ile Glu Arg Met Asn Ser Ile His  
340 345 350  
Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Glu Thr Leu Cys Cys  
355 360 365  
Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile Ile Asp Ser Glu Tyr Thr  
370 375 380  
Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala  
385 390 395 400  
Ile His Phe Gly Val Phe Thr Ile Lys Ala Asp Val Trp Ser Phe Gly  
405 410 415  
Val Leu Leu Met Val Ile Val Thr Tyr Gly Arg Val Pro Tyr Pro Gly  
420 425 430  
Met Ser Asn Pro Glu Val Ile Arg Ser Leu Glu His Gly Tyr Arg Met  
435 440 445  
Pro Cys Pro Glu Thr Cys Pro Pro Glu Leu Tyr Asn Asp Ile Ile Thr  
450 455 460

X

Glu Cys Trp Arg Gly Arg Pro Glu Glu Arg Pro Thr Phe Glu Phe Leu  
465 470 475 480

Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Glu  
485 490 495

Leu Gln Pro

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGAATTCCTCA CAGNGACTTN GCNGCNAG

28

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCCTCA ANGTCANAC GTCNGA

26

B3  
cancel

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